

Input Set: I512363.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Ni, Jian
2 Ruben, Steven M.
3 <120> TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
4 TR11, TR11SV1, and TR11SV2
5 <130> FILE REFERENCE: PF396
6 <140> CURRENT APPLICATION NUMBER: US/09/512,363
7 <141> CURRENT FILING DATE: 2000-02-23
8 <150> EARLIER APPLICATION NUMBER: 60/063,212
9 <151> EARLIER FILING DATE: 1997-10-21
10 <150> EARLIER APPLICATION NUMBER: 09/176,200
11 <151> EARLIER FILING DATE: 1998-10-21
12 <150> EARLIER APPLICATION NUMBER: 60/121,648
13 <151> EARLIER FILING DATE: 1999-02-24
14 <150> EARLIER APPLICATION NUMBER: 60/134,172
15 <151> EARLIER FILING DATE: 1999-05-13
16 <150> EARLIER APPLICATION NUMBER: 60/144,076
17 <151> EARLIER FILING DATE: 1999-07-16
18 <160> NUMBER OF SEQ ID NOS: 28
19 <170> SOFTWARE: PatentIn Ver. 2.0
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21 <211> LENGTH: 983
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (118)..(819)
27 <220> FEATURE:
28 <221> NAME/KEY: mat_peptide
29 <222> LOCATION: (193)..(819)
30 <220> FEATURE:
31 <221> NAME/KEY: scRNA
32 <222> LOCATION: (118)..(192)
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35 cgggtgagga cggggacggg gcgtgtccaa ctggctgtgg gctttgaaa cccgagc 117
36 atg gca cag cac ggg gcg atg ggc gcg ttt cgg gcc ctg tgc ggc ctg 165
37 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
38 -25 -20 -15 -10
39 gcg ctg ctg tgc gcg ctc agc ctg ggt cag cgc ccc acc ggg ggt ccc 213
40 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
41 -5 -1 1 5
42 ggg tgc ggc cct ggg cgc ctc ctg ctt ggg acg gga acg gac gcg cgc 261
43 Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg
44 10 15 20

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45 tgc tgc cgg gtt cac acg acg cgc tgc tgc cgc gat tac ccg ggc gag 309
46 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
47 25 30 35
48 gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac 357
49 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
50 40 45 50 55
51 tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca 405
52 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
53 60 65 70
54 ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt 453
55 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
56 75 80 85
57 atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc 501
58 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
59 90 95 100
60 aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct 549
61 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
62 105 110 115
63 ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca 597
64 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
65 120 125 130 135
66 gag ccg ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc 645
67 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
68 140 145 150
69 gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg 693
70 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
71 155 160 165
72 agg aag acc cag ctg ctg gag gtg ccg ccg tcg acc gaa gac gcc 741
73 Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
74 170 175 180
75 aga agc tgc cag ttc ccc gag gaa gag cgg ggc gag cga tcg gca gag 789
76 Arg Ser Cys Gln Phe Pro Glu Glu Arg Gly Glu Arg Ser Ala Glu
77 185 190 195
78 gag aag ggg cgg ctg gga gac ctg tgg gtg tgagcctggc cgtcctccgg 839
79 Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
80 200 205
81 ggccaccgac cgccaggcccccag ccctccccag gagctccccca ggccgcaggc gctctgcgtt 899
82 ctgctctggg ccggggccctg ctccccctggc agcagaagtg ggtgcaggaa ggtggcactg 959
83 accagcgccc tgaccatgc agtt 983
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85 <211> LENGTH: 234
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
88 <400> SEQUENCE: 2
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91 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
92 -5 -1 1 5
93 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
94 10 15 20

Input Set: I512363.RAW

95 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
96 25 30 35
97 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
98 40 45 50 55
99 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
100 60 65 70
101 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
102 75 80 85
103 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
104 90 95 100
105 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
106 105 110 115
107 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
108 120 125 130 135
109 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
110 140 145 150
111 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
112 155 160 165
113 Arg Lys Thr Gln Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala
114 170 175 180
115 Arg Ser Cys Gln Phe Pro Glu Glu Arg Gly Glu Arg Ser Ala Glu
116 185 190 195
117 Glu Lys Gly Arg Leu Gly Asp Leu Trp Val
118 200 205

119 <210> SEQ ID NO 3

120 <211> LENGTH: 1007

121 <212> TYPE: DNA

122 <213> ORGANISM: Homo sapiens

123 <220> FEATURE:

124 <221> NAME/KEY: CDS

125 <222> LOCATION: (121)..(843)

126 <400> SEQUENCE: 3

127 gtcgaccac gcgtccgggg ggccacccct gggtcctgca ggggcagctc ctggttgcat 60
128 atggaggtag cacctggca gggcagctg tggggcgcaa agggggagta gccaggccac 120
129 atg gcc cca gga gaa aga gac agc tgg ata aac cca ggt cca gac tcc 168
130 Met Ala Pro Gly Glu Arg Asp Ser Trp Ile Asn Pro Gly Pro Asp Ser
131 1 5 10 15
132 cag cca gga gcc ctc tgc tcc ctg gag cca act gtg ggt gga gaa cgg 216
133 Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg
134 20 25 30
135 aca acc tca ctc ccc tgg agg gcc gag ggg agg cct ggg gag gag ggg 264
136 Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Gly
137 35 40 45
138 gcc tca gcc cag ctg ctg ggg ggc tgg cct gtc tcc tgc cca ggc gag 312
139 Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu
140 50 55 60
141 gag tgc tgt tcc gag tgg gac tgc atg tgt gtc cag cct gaa ttc cac 360
142 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
143 65 70 75 80
144 tgc gga gac cct tgc tgc acg acc tgc cgg cac cac cct tgt ccc cca 408

Input Set: I512363.RAW

145 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
 146 85 90 95
 147 ggc cag ggg gta cag tcc cag ggg aaa ttc agt ttt ggc ttc cag tgt 456
 148 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
 149 100 105 110
 150 atc gac tgt gcc tcg ggg acc ttc tcc ggg ggc cac gaa ggc cac tgc 504
 151 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
 152 115 120 125
 153 aaa cct tgg aca gac tgc acc cag ttc ggg ttt ctc act gtg ttc cct 552
 154 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
 155 130 135 140
 156 ggg aac aag acc cac aac gct gtg tgc gtc cca ggg tcc ccg ccg gca 600
 157 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
 158 145 150 155 160
 159 gag ccg ctt ggg tgg ctg acc gtc gtc ctc ctg gcc gtg gcc gcc tgc 648
 160 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
 161 165 170 175
 162 gtc ctc ctc ctg acc tcg gcc cag ctt gga ctg cac atc tgg cag ctg 696
 163 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
 164 180 185 190
 165 agg agt cag tgc atg tgg ccc cga gag acc cag ctg ctg ctg gag gtg 744
 166 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val
 167 195 200 205
 168 ccg ccg tcg acc gaa gac gcc aga agc tgc cag ttc ccc gag gaa gag 792
 169 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu
 170 210 215 220
 171 cggttggc gag cga tcg gca gag gag aag ggg cgg ctg gga gac ctg tgg 840
 172 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
 173 225 230 235 240
 174 gtgttggc cgttcctccgg ggccaccgac cgcagccagc ccctccccag 893
 175 Val

W-->

176
 177 gagctccccca ggccgcagg gctctgcgtt ctgctctggg ccggggccctg ctccccctggc 953
 178 agcagaagtg ggtgcaggaa ggtggcagtg accagcgccc tggaccatgc agtt 1007
 179 <210> SEQ ID NO 4
 180 <211> LENGTH: 241
 181 <212> TYPE: PRT
 182 <213> ORGANISM: Homo sapiens
 183 <400> SEQUENCE: 4
 184 Met Ala Pro Gly Glu Arg Asp Ser Trp Ile Asn Pro Gly Pro Asp Ser
 185 1 5 10 15
 186 Gln Pro Gly Ala Leu Cys Ser Leu Glu Pro Thr Val Gly Gly Glu Arg
 187 20 25 30
 188 Thr Thr Ser Leu Pro Trp Arg Ala Glu Gly Arg Pro Gly Glu Glu Gly
 189 35 40 45
 190 Ala Ser Ala Gln Leu Leu Gly Gly Trp Pro Val Ser Cys Pro Gly Glu
 191 50 55 60
 192 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
 193 65 70 75 80
 194 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro

Input Set: I512363.RAW

195 85 90 95
 196 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
 197 100 105 110
 198 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
 199 115 120 125
 200 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
 201 130 135 140
 202 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
 203 145 150 155 160
 204 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
 205 165 170 175
 206 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
 207 180 185 190
 208 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
 209 195 200 205
 210 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
 211 210 215 220
 212 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
 213 225 230 235 240
 214 Val
 215 <210> SEQ ID NO 5
 216 <211> LENGTH: 1074
 217 <212> TYPE: DNA
 218 <213> ORGANISM: Homo sapiens
 219 <220> FEATURE:
 220 <221> NAME/KEY: CDS
 221 <222> LOCATION: (1)..(720)
 222 <220> FEATURE:
 223 <221> NAME/KEY: sig_peptide
 224 <222> LOCATION: (1)..(57)
 225 <220> FEATURE:
 226 <221> NAME/KEY: mat_peptide
 227 <222> LOCATION: (58)..(720)
 228 <400> SEQUENCE: 5
 229 atg ggc gcg ttt cgg gcc ctg tgc ggc ctg gcg ctg ctg tgc gcg ctc 48
 230 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
 231 -15 -10 -5
 232 agc ctg ggt cag cgc ccc acc ggg ggt ccc ggg tgc ggc cct ggg cgc 96
 233 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
 234 -1 1 5 10
 235 ctc ctg ctt ggg acg gga acg gac gcg cgc tgc tgc cgg gtt cac acg 144
 236 Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
 237 15 20 25
 238 acg cgc tgc tgc cgc gat tac ccg gcc cag ctg ctg ggg ggc tgg cct 192
 239 Thr Arg Cys Cys Arg Asp Tyr Pro Ala Gln Leu Leu Gly Gly Trp Pro
 240 30 35 40 45
 241 gtc tcc tgc cca ggc gag gag tgc tgt tcc gag tgg gac tgc atg tgt 240
 242 Val Ser Cys Pro Gly Glu Glu Cys Cys Ser Glu Trp Asp Cys Met Cys
 243 50 55 60
 244 gtc cag cct gaa ttc cac tgc gga gac cct tgc tgc acg acc tgc cgg 288

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I512363.RAW

Line	?	Error/Warning	Original Text
176	W	Invalid/Missing Amino Acid Numbering	
384	W	"N" or "Xaa" used: Feature required	cgattAACCC ggggcgaaga atngtggtt ccgagtn gccttgaat tccaattgcg gaagaaccct tngctgc
385	W	"N" or "Xaa" used: Feature required	acctttgttc ccccaaAGCC naagggggta anaattcc
386	W	"N" or "Xaa" used: Feature required	ggccgagggg aggcctgggg aggagggggc ctcagccc
452	W	"N" or "Xaa" used: Feature required	ctcctgccc ggcgaggant gctgttccga gtggaaat
453	W	"N" or "Xaa" used: Feature required	ccattgcga gaaccttgct gcacgaattt cccggcaac
454	W	"N" or "Xaa" used: Feature required	ggttnacattt ccaggggaan ttcatTTTT gnttccat
455	W	"N" or "Xaa" used: Feature required	ttntccgggg gccanaaggc aatgaaaaac ttgganaa
456	W	"N" or "Xaa" used: Feature required	ttccnnggaa aagaccanaa gttttggtc caggtccc
457	W	"N" or "Xaa" used: Feature required	

Input Set: I512363.RAW

PREVIOUSLY ERRORED SEQUENCES-EDITED

1 <210> 28
2 <211> 241
3 <212> PRT
4 <213> Homo sapiens
5 <400> 28
6 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
7 1 5 10 15
8 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
9 20 25 30
10 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
11 35 40 45
12 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
13 50 55 60
14 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
15 65 70 75 80
16 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
17 85 90 95
18 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
19 100 105 110
20 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
21 115 120 125
22 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
23 130 135 140
24 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
25 145 150 155 160
26 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
27 165 170 175
28 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
29 180 185 190
30 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
31 195 200 205
32 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
33 210 215 220
34 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
35 225 230 235 240
36 Val